

SEQUENCE LISTING



<110> GONG, Zhiyuan  
LAM, Toong Jin  
JU, Bensheng  
XU, Yanfei  
HE, Jiangyan  
YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT  
TRANSGENIC ORNAMENTAL FISH

<130> 1781-0163P

<140> 09/913,898

<141> 2001-08-17

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<151> 1999-01-14

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Leu Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Gln Ala Val Arg  
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Thr Ser Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe  
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 Ala Thr Ile His Val Gln Gln Thr Ser Gly Gly Val Ser Ser Gly Tyr  
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Gly Gly Ser Gly Ser Gly Phe Gly Tyr Ser Ser Gly Phe Ser Ser Gly  
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 Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys  
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cac aac aac cac atg gcc aag gtg ctg act aag gaa atg tat ggc aag 208  
 His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys  
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ctt agg gac aag cag acc cca cct gga ttc act gtg gat gat gtc atc 256  
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Gln Leu Ile Ala Asp His Phe Leu Phe Asp Lys Pro Val Ser Pro Leu			
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ctg ctg gct gct ggt atg gcc cgt gac tgg ccc gat gcc aga ggc att			736
Leu Leu Ala Ala Gly Met Ala Arg Asp Trp Pro Asp Ala Arg Gly Ile			
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Trp His Asn Glu Asn Lys Ala Phe Leu Val Trp Val Lys Gln Glu Asp			
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His Leu Arg Val Ile Ser Met Gln Lys Gly Gly Asn Met Lys Glu Val			
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Phe Lys Arg Phe Cys Val Gly Leu Gln Arg Ile Glu Glu Ile Phe Lys			
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Lys His Asn His Gly Phe Met Trp Asn Glu His Leu Gly Phe Val Leu			
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Val Leu Thr Lys Glu Met Tyr Gly Lys Leu Arg Asp Lys Gln Thr Pro  
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Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro  
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Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu  
 65 70 75 80

Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg  
 85 90 95



His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe  
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Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser  
115 120 125

Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro  
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His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu  
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Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu  
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Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe  
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Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Leu Ala Ala Gly Met Ala  
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Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Glu Asn Lys Ala  
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Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met  
225 230 235 240

Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly  
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Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly  
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 Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met  
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Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala  
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Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro  
65 70 75 80

His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr  
85 90 95

Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg  
100 105 110

Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr  
115 120 125

Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr  
130 135 140

Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu  
145 150 155 160

Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn  
165 170 175

Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile  
180 185 190

Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp  
195 200 205

Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn  
210 215 220

Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile  
225 230 235 240

Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val  
245 250 255

Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu  
260 265 270

Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr  
275 280 285

Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu  
 290 295 300

Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp  
 305 310 315

<210> 7  
 <211> 2241  
 <212> DNA  
 <213> Danio rerio

<220>  
 <221> TATA signal  
 <222> (2103)..(2108)

<220>  
 <221> primer\_bind  
 <222> (2221)..(2241)  
 <223> CK2

<220>  
 <221> misc\_feature  
 <222> (2142)..(2235)  
 <223> Identical to the 5' CK cDNA

<400> 7  
 ccttcccttc tacttttgac gtccttttaa gagcttgtgc atgaaagcag atttggagct 60  
 gattactcat ctcaaacacc catacaaagg gatgattgcc gtaccatgat ctacacacct 120  
 tcacacctgg ttatactat gatagttgta gacgattgcg taatgctatt aaatgcccat 180  
 cagtgtctggc tgtgacaccc aactgctgcc atttcgtgtt gacttgcacg agaaatgaga 240  
 aattgtctga ctatgcaggg tgtctatgcg tgggaacatt tatcagtggt cattaaatac 300  
 tatagtttac agttagacca aagtgtgctg tatttttgtg ttagcttagc tgcagttttt 360  
 gtgtgtgaag taacaaatga caaatactca aactattgta attaagtagt ttttctcaga 420  
 aattgtaatt tactaagtag tttaaaaatg tgtactttta ctttcccttg agtacatttt 480  
 tagtgcagtg ttggtacttt tatttcaact ccttccctca acctgcagtc actactttat 540  
 ttattcttgt ctatgtggat tagacaaatc agtcctgtga ttctgtcca atcaaattgc 600  
 acatagaagg taaatcacat cataatgaac taccttaaga catgggccat ttataattgc 660  
 agcaaactgt ttgccagcat taaaagaaga tgtcaaaaat atttacacgc attaacccag 720  
 agactgctta gatgcatgac actgatgaga agatgatgga tgtttactgt atgatgaccg 780  
 aaataacttt aaacgcacac aagacggcac aagacgtcaa catggcgtaa ggttgacgtt 840  
 gtacccaac gcagtgggga cggtgcattt tgtttagaaa tgaaaattag gttgacgtca 900  
 gaactcaacg tcaggtcgat gtcaatgttc aacatccaat ctaaaatcat atatcaatgt 960  
 ctaatgatgt tacagcttga tgttatgcgg atgttacctt tatgacgtct atcagacgtt 1020  
 ggattatggg tgccataacct gatgaataaaa tgtcattatt tgacgttggg ttaagatgtt 1080  
 ggttcgacat tggatttttg tgcgtttcca acacaacctt aatccaccaa atattaactt 1140  
 cctatgacat cgttatttga cgtcaaaaata acaatatcct tagatgctgg ctgacttttg 1200  
 aatttaggtc accacaacct atatttaacc taatattaac atcttatgat gttgtgtgcc 1260  
 tgtggggcaa taactaaatg cactacagaa tgttacgttt acacacatgt aaattacatg 1320  
 taaatgcatc agcttttcac agcataatc tcaactacta ctactcttga gtacttttaa 1380  
 aaaagctact tttcaactcat actttgagta atattttaca ctgatacttt tactcgcaact 1440  
 acatttttag gcatgtattg atatttttac tatgattttt cagtactctt tccactactg 1500  
 cagccctccc catacataat cgtatgttta cacatatggg ggagtttaga gccataatct 1560  
 acattagctt tgttagccgc tagcattact gtgcagaatt gtgtgtgtgc acattttcca 1620  
 atatcaatac agaaggaaac tgtgttcctt gttcccttgt aaatctcaac aatgcaactg 1680  
 ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaaaag tgaatggaaa 1740  
 aaagcctttc attaatgtga aagttgtctg gcgccccacc cagataaaaa gagcagaggt 1800

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taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca caccgcgtgg 1860
cagatgggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
ctcaagcctc tccttgcatc ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
caacatttat cttaccactt tctctctgta cctgtctaac aggtagggtg tgtgtgagag 2040
tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtcg gctccaccct ctcaagagt 2100
tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
tgagcaacct cctccactca ctctctctc agagagcact ctctgtacctc cttctcagca 2220
actcaaagac acaggatccg g 2241

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<210> 8
<211> 1456
<212> DNA
<213> Danio rerio

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<220>
<221> TATA_signal
<222> (1389)..(1394)

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<220>
<221> primer_bind
<222> (1433)..(1456)
<223> MCK2

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<220>
<221> misc_feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA

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<400> 8
gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
tgtggcttaa tcttggctga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
gcatgtgcac catgacaggc ctgttattca cacttgggtg catgttggag actgttcggc 180
cagctatagt tttcttcaca gagtcctggg tcacctaatg tcacaaggaa gaaacatgtt 240
acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accaggggagg ggttttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc ttaaaagaag 480
acacaacagg gatagttcac ccaaaaaaca gaccattctt tttttctgtt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
aagtcaatgg gtcttccagc attttttcaa tataccttac tttgagttca aaagaaaaac 660
acatctcaaa taggtttgag gttgaataaa catttttcat tttgggtgtg actatcccta 720
attatttgac acttaagatt tatagtaaat cattttatag actttctccc cttattaaac 780
atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccctg 840
tcaaatgttt ttgtgtatgg ttggcgcaca atagactgaa ctggcctatc acacagactt 900
tcataacaac tccagttgat gccctttcac cctcagtgtg taaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagtttgac 1020
ccagaatcat gtgtgaacg aagcctacca agagattttt gaaagccatc ggctgacac 1080
gcgcacttct gatatctgtg gtatgttttg caaaagtgtc gctcagcctt tttagcatgg 1140
cagatcctcc acatcccac accctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccacac gctgccacct 1260
catctaggat gcctggggcc taaattgaag cctttcttac actaaacagg gcataagaga 1320
ccagcggccag ccaatcataa ttcagtgagc tctaaaatgg gccagccaat ggctgcagg 1380
gctagaggta tatatatcca aatcaaactc ttcttgcttg ggtgaccctc atttcggctt 1440
ggtgaacagg atccgg 1456

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<210> 9  
 <211> 2205  
 <212> DNA  
 <213> Danio rerio

<220>  
 <221> primer\_bind  
 <222> (2179)..(2205)  
 <223> ARP2

<220>  
 <221> misc\_feature  
 <222> (2153)..(2199)  
 <223> Identical to the 5' ARP cDNA

<220>  
 <221> intron  
 <222> (792)..(2152)

<220>  
 <221> misc\_feature  
 <222> (775)..(791)  
 <223> Identical to the 5' ARP cDNA

<400> 9  
 atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgac 60  
 attttaattt gtgttgtata attttacatt ttgtaagtat tatttttata aaaaatatat 120  
 agaaataata caaatttggtt tacagtattc ttagttattg caataaacga attttatata 180  
 gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240  
 tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300  
 agataataaa gtgacttttt tgggcggacc aaatttcctt attaatggc aattcattaa 360  
 aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420  
 gtgcagattt ttggctgttg ttagaaggga tacatctgcg gccgaaagt aacgggaact 480  
 atttacattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540  
 tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatc 600  
 tatattgacc gcagctgtat cttttctaag tgcgactgta caaatacgca ctgaccgtga 660  
 cagacacgtg cattgaccaa tcagcgcaca gatacgcat ttccgcgcga ttctgattgg 720  
 atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctctttct ttcacgcgtc 780  
 cctaccgtga ggtaaggctg acgccgctct tgtggcgggt tcttaaaatg tgtaataaaa 840  
 taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900  
 tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgttagca 960  
 caggcctcgt gcgccatgtg tgacgcgacg ttttaatatg atcttatttg attttgatga 1020  
 tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080  
 ttacatgcta gtacttgtgc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140  
 ttttaaaacc agttactctc attttagtga aatattctta agccactaag ttaaaatttg 1200  
 tcaatcacat ataatttgtt ttatgtttta tttgagtcac cataccagg aatagtttta 1260  
 tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320  
 gtaaagttaa tcttaaaggg gtaaaggctc acccaaaaga caattcacgg tcaagtgttt 1380  
 tcaaattctt tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440  
 accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500  
 ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560  
 tgcataaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620  
 gcagtgggtc ccaagcttgt tcctgaaggg ccagtgtcct acagatttta gctccaaccc 1680  
 taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740  
 gcagggtgtg tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800  
 gtgacccttg cctcaagcca tcacaaatgc attatgggat taagaaatgt gcaggttcag 1860  
 ttatggacag gctgttgcag tgcttgttcg tcgttccac tgcacaaatg aacatgattc 1920

cttctatccc tgtctgtctg catctcatga cttgcaggga cgctgggtctc agacacgttt 1980  
 atagcagtaa atcaaataca atagtgtctt gattatcttt aaatatttga aagcttataa 2040  
 taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaat 2100  
 aagatgcaca caaggcaggt gtaaaagtat tgcttggtgt tgtaatcctc agattttaca 2160  
 accttgctct taaaccggct gttcacccgat ccttgggaagg gatcc 2205

<210> 10  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Cytokeratin  
 gene specific primer

<400> 10  
 cgctggagta agagatagac ctgg 24

<210> 11  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Cytokeratin  
 gene specific primer

<220>  
 <221> misc\_feature  
 <222> (1)..(6)  
 <223> Introduced for restriction site

<220>  
 <221> misc\_feature  
 <222> (3)..(8)  
 <223> BamHI site

<400> 11  
 ccggatcctg tgtctttgag ttgctg 26

<210> 12  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Muscle  
 creatine kinase gene specific primer

<220>  
 <221> misc\_feature  
 <222> (3)..(8)  
 <223> BamHI site



<400> 12  
ccggatcctt gggatcagat cctg

24

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Muscle  
creatine kinase gene specific primer

<220>  
<221> misc\_feature  
<222> (1)..(3)  
<223> Introduced for restriction site

<220>  
<221> misc\_feature  
<222> (3)..(8)  
<223> BamHI site

<400> 13  
ccggatcctg ttcaccaagc cgaa

24

<210> 14  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Acidic  
ribosomal protein PO gene specific primer

<400> 14  
tagttggact tccacgtgcc ctgtc

25

<210> 15  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Acidic  
ribosomal protein PO gene specific primer

<220>  
<221> misc\_feature  
<222> (1)..(7)  
<223> Introduced for restriction site

<220>  
<221> misc\_feature

<222> (1)..(6)  
<223> BamHI site

<400> 15  
ggatcccttc caaggatcgg tgaaca

26

<210> 16  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide for linker used in linker-mediated  
PCR

<400> 16  
gttcacatcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c

51

<210> 17  
<211> 10  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide for linker used in linker-mediated  
PCR

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> n is a dideoxycytidine

<400> 17  
gaattcaagn

10

<210> 18  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: linker  
specific primer

<400> 18  
gttcacatcttt acaagctagc g

21

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: linker  
specific primer

<400> 19  
tcctgaacaa tgctgtggac

20

<210> 20  
<211> 1392  
<212> DNA  
<213> Danio rerio

<220>  
<221> CDS  
<222> (42)..(551)

<220>  
<221> primer\_bind  
<222> (6)..(28)  
<223> M2

<220>  
<221> primer\_bind  
<222> (23)..(45)  
<223> M1

<220>  
<221> polyA\_signal  
<222> (797)..(802)

<220>  
<221> polyA\_signal  
<222> (1351)..(1357)

<400> 20  
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Met Ala Pro Lys Lys  
1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104  
Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser  
10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152  
Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile  
25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200  
Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp  
40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248  
Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu  
55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296  
 Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu  
 70 75 80 85  
  
 acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344  
 Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile  
 90 95 100  
  
 gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392  
 Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys  
 105 110 115  
  
 aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440  
 Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr  
 120 125 130  
  
 gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488  
 Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala  
 135 140 145  
  
 ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536  
 Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu  
 150 155 160 165  
  
 gag aag gag gag taa acaaccttgg aatcaagaaa acgaagagaa gaacatgcat 591  
 Glu Lys Glu Glu  
  
 cctcacagct taatctccag tctgttgtct ggctttctct aacttttgtt tttccttcc 651  
 ccctttcttg ctttctacca tcgttggttac tccaagcact tacactctcc atcttacc 711  
 agacttgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771  
 cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt 831  
 ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag 891  
 cttgcatgta agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta 951  
 tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga 1011  
 aagaagcacg atggagtgat ctactctat aatagaggaa ccagtcatca ttctcatttc 1071  
 ctctctggt ggttgactaa aaagagaaaag agaaaatgag ggttttgtgc tgagtgaagt 1131  
 tagctccta aaagcgatgc cgagctcatc acagaggagg tgagaggggac agaccatcct 1191  
 aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccc 1251  
 cctcttctct atttctctgt ccatcttttc ttttttcttt tttctttttt gctttctgca 1311  
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 aataaaaaaa aaaaaaaaa a 1392

<210> 21  
 <211> 169  
 <212> PRT  
 <213> Danio rerio

<400> 21  
 Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser  
 1 5 10 15  
  
 Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys  
 20 25 30  
  
 Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys  
 35 40 45

Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys  
50 55 60

Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn  
65 70 75 80

Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp  
85 90 95

Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly  
100 105 110

Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln  
115 120 125

Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe  
130 135 140

Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val  
145 150 155 160

Ile Thr His Gly Glu Glu Lys Glu Glu  
165

<210> 22  
<211> 2054  
<212> DNA  
<213> Danio rerio

<220>  
<221> TATA\_signal  
<222> (1983)..(1989)

<220>  
<221> enhancer  
<222> (142)..(148)  
<223> E-box, canntg

<220>  
<221> enhancer  
<222> (452)..(457)  
<223> E-box, canntg

<220>  
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<222> (1095)..(1100)  
<223> E-box, canntg

<220>  
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<222> (1278)..(1283)  
<223> E-box, canntg

<220>  
<221> enhancer

<222> (1362)..(1367)  
 <223> E-box, canntg  
  
 <220>  
 <221> enhancer  
 <222> (1385)..(1390)  
 <223> E-box, canntg  
  
 <220>  
 <221> enhancer  
 <222> (523)..(532)  
 <223> Potential MEF2 binding site, yta(w)4tar  
  
 <220>  
 <221> enhancer  
 <222> (606)..(615)  
 <223> Potential MEF2 binding site, yta(w)4tar  
  
 <220>  
 <221> enhancer  
 <222> (697)..(706)  
 <223> Potential MEF2 binding site, yta(w)4tar  
  
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 <221> enhancer  
 <222> (1490)..(1499)  
 <223> Potential MEF2 binding site, yta(w)4tar  
  
 <220>  
 <221> enhancer  
 <222> (1640)..(1649)  
 <223> Potential MEF2 binding site, yta(w)4tar  
  
 <220>  
 <221> enhancer  
 <222> (1956)..(1965)  
 <223> Potential MEF2 binding site, yta(w)4tar  
  
 <220>  
 <223> Transcription start site at residue 2012  
  
 <220>  
 <221> primer\_bind  
 <222> (2032)..(2054)  
 <223> M2  
  
 <220>  
 <221> misc\_difference  
 <222> (2027)..(2054)  
 <223> Identical to the 5' MLC2f cDNA

<400> 22  
 tgcattgcctg gcaggtccac tctagaggac tactagtcatt atgcgattct gaacaattgct 60  
 gtggacagct tgaattcaat tcgccacaga ggaatgagcc accaactcat ccagtgtatt 120  
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